

SEQUENCE LISTING

<110> BENOIT, Patrick  
SCHWARTZ, Bertrand  
BRANELLEC, Didier  
CHIEN, Kenneth R.

<120> SEQUENCES UPSTREAM OF THE CARP GENE, VECTORS CONTAINING  
THEM AND USES THEREOF

<130> 03806.0530-00000

<140>

<141> 2001-12-07

<160> 5

<170> PatentIn Ver. 2.1

<210> 1

<211> 2358

<212> DNA

<213> *Mus musculus*

<400> 1

ggatcctttc atgttaaca atatcaaccc taacccaagg ggaacagcct gcctgacagt 60  
ggcttgcca cccatgaata cttcctagtc tagtccgttt gtgaaactca gccccatccca 120  
acacttctgc aagccccatc ctctacaagg tgctcattgg gaatttcctg gagcttctct 180  
ttcaggatca gcctgattct agggcagcag ttctcaacct gggggcctcg acccccttgg 240  
ggaaatcaa cgacccttta caggggtcac atatcatcta tcctatatgt caggtattta 300  
cattacgatt cgtaacagta gcaaaattac agtatgaaa tagcaatgaa ataattttat 360  
gattgaaggt caccacaaca tgaggccgcc acactgttct agagaaaaat cacctgggtg 420  
ggaaagggtt tggaaagcc tttctgtcca ttcttcattc ttcaaagtga tgtgttcaca 480  
gaaagccttt cagctgttct gctggggctc ttagtaagtc tgagtaggaa ctgtatgtac 540  
caggtctgct tcttatgggt ggagccaaga cgcatcgtgg gtggagcga gacgcaacct 600  
cacttcttag ctctgcattcc atagcaagta gcctaatttt tctgtgtcta ggtgtcatct 660  
ctgtgaatcg agatccttgg cttgtttga attagggagg cacaaaatac tcagagattc 720

aagactgctc agcagccag agtccttcct caaaggaaag gtctcaactc tcagcccccc 780  
ttagctctga gtcaggcctg gaacaaacgg ccacaggaat gagaaaagct gccatagctg 840  
cttgcactt caagaggta aagaaaatag tgttaaccat gaaaacgaga agaccaacag 900  
ttatccattt atagcgtctc aggacagata ggacagagag aacacttagga gagggaaacc 960  
cacgaaggac aaggtattag tgtgttggtt ttcagggcaa tgtcttgcac tgaagattct 1020  
agaaacacaa tttgctggtt gaacagctga agtgggggtgg gggttcttac cccatgttca 1080  
tggaaagggtg agtgaggaga gacagatata tgcgttgcag cataacaaac atacacaaca 1140  
ccctaattaa cactccctc ttctactgac acccccttca ctctcctctt tcataaaaaaa 1200  
taaaaaaaagt attttatgtg gctcttacga tagaatcttt cctcgaacta taaaaagatc 1260  
taaatattta tattttcac attttaatat ctttagcgatg acaagccaga aacaagtatt 1320  
ttttgcctct ctcaacagca aagcttgggg ccttttggtt tccgttgcac taaatagaaca 1380  
cgagagcccc gtgtatctag gcagatgctc tatttcatttc ccatgagtct ccagcctcag 1440  
acgcacattt ttctcggct ctcttaagct tttccacag cattggaaa ctttactgac 1500  
agcatccaag ttgtgcttct gctaagaact ggactcacat ctctctgtgc atcacttcgg 1560  
ccgttttgg ggttagatcct ctgatttagcc ttcagattta gaacacggtg agcctgtgg 1620  
ugcactaatta tggccagtgta caccatagag tcaaagtgc tttactgaatg ctttcaattt 1680  
ctcctaatttc tggtagatg gcatgtcaca gggccatttt agctgcagac atcactccag 1740  
agaattccaa acagatagag acaagtggca cccagaccca tctccttccc ctcggctga 1800  
ttatccccag aaataggatg tcccaaagca acacttccca gccaacttggaa gtgctgataa 1860  
gtccagttat cagaaagata tggctgttaag tgtgtatgcac agtgcattgc ttttcttgat 1920  
acgttagtca tatgagagct gacaaagaag gaaaaagagc agcgatgtgg tgcaatattt 1980  
acaggcagct gtccccctggc ttcccgatac gtgggatgac tcgcattgc gagcgggttg 2040  
gtcactgcca aaggaatgac cctctcacat ttcttcctga ttgcatacg ccgcggccag 2100  
cttgcattct ccctcttggg cttcccgatac actaagtctg gaatgaaaat tcacctgcct 2160  
ctgaatttggc cactgggtgg ggcagggggtg tgacttggct tcccaggctg gaagatttac 2220  
tcacccagcc ctagctatat aacgggctgg tgtggagggg ctccacaggg ccagttccag 2280  
gggttcatcc acaagagaga aaaacataga ctgcgggtct agggagcttgc catgcctgca 2340

ggtcggaggc caccatgg

2358

<210> 2  
<211> 2074  
<212> DNA  
<213> Homo sapiens

<400> 2  
ctgcagcaag ttacttaatg tttttgcct cagcatcctc tctgtaaaat gagagcatta 60  
gtcttgctcc aacttcgagg gcatggacag ctctgggatt tcatatccaa gacccttaaa 120  
catcccacag tccttcccccc aaacacttct cctcctaata cctccctcag tttgggtcag 180  
gcctggaaca aaaaggcata cgaaatggta gaaaaagtgt ccatgactac ttctgactta 240  
gatgaagaga ccaatgaaaa tagtaatgac tctgttgct tcagcaggac atatactaaa 300  
ataggagcta tacaaagaag attagcatgg actctgtgca agaatgacac acaaatttgt 360  
gaaacattcc atatattaaa aataaataaaa taataaagag aaaaggaaaa aattaaaaag 420  
aaaatagtga tagctgtgtc catctcaaag aaaagcccag gagatttcct ttatttaccc 480  
cctttaagat agaatattag gagaccggaa catatgatac aggaggtact gggagggtcc 540  
ctctttgtca atgtttgtc ttgggggtggg gagtcgatgt cttctcaaag tttcagaaac 600  
accatccact gactgagcat tcaaggggca agaggagaat ggcagccaca tttgttgatt 660  
gggtgagttt ggggagaaat agacacacaa agtcaaaca taacttccta attaacactt 720  
ccctccattc acaattccct tctccattc ttctctcctg tctttacts akaraaaccc 780  
agttttcct gaaactataa aaatacccccc agtatgttta cataatttac acctcaaaga 840  
ttagaaacca gaaatagaga cctttcaac cttccggaa gcaaagtgca ttatccctcc 900  
agccacgtgt ctcaaatctt gatgcatcag aatcatctgg gtgcattkaa attcaagatg 960  
attcctacga gttaccataa atcaactcag aattccctgg agtggggcca gggatctgta 1020  
tttctgacaa gctcccacag gtgattcctt tccccacagc atttgagaac ttcagctcaa 1080  
tgacctaatac agagtccctgc cattgcta atctggtctc attttbtca tatatatata 1140  
tagtatttgt ggttagagatg ggattttgcc atgttgccca ggctagtatt gaactcctaa 1200  
gctaagcaat cttcctgtct ctgcctccca aaatgttggg attacaggtg taagccactg 1260

caccggctg atagctggtt tcatttactc tatttcttga ccactctgat ccattttgaa 1320  
gtaaaaatgc tccaattatt atgctgtttt agaacacggt aagcatgtca tgtgctaatg 1380  
gccagtgaca tcataaaaga aaagtgcatt actgaatgct ttcaatgtct tataatgatg 1440  
gtaaggtggc atgtcatggg gcctatttag cccagacatc actccaaaga attccaaaca 1500  
gatatagaca agtgcctta gggcccagat ccctccccc caggctgttt acccaggaa 1560  
taggatgtcc tgggacaagt ttcccctaag tgaagtgtt gataagtctgc ttatcagaaa 1620  
gatattactg ggggtgtgat atgttagggca tctacatttt cttgataggt agtcatatga 1680  
aagctgacaa agaaaaaaag ggcagtgtatg tggtgcaatg tcaacagaca gctgtccct 1740  
gactcttgc acataggatg acttgcattt ctgagcgatg tgcatttgc caaaggaatg 1800  
gccctctcac atttcttcc gattcacata ttcagcaggg ttagcttgc ctccctccc 1860  
tcttcagctt cccagacact gagtctggaa tgaaaattca cctgcctctg agttggctcc 1920  
taatgggggc gggagtgtta cttcggttcc caggttggaa gattatctca cccggccca 1980  
gctatataag ctgaccggtg tggaggggcc cagcagggcc aactccaggg attccttcca 2040  
cgacagaaaa acatacaaga ctcccttcagc caac 2074

<210> 3  
<211> 750  
<212> PRT  
<213> Homo sapiens

<400> 3  
Met Gly Glu Thr Leu Gly Asp Ser Pro Ile Asp Pro Glu Ser Asp Ser  
1 5 10 15  
Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Met Thr Met Val  
20 25 30  
Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val  
35 40 45  
Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro  
50 55 60  
Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp  
65 70 75 80  
Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp  
85 90 95

Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser  
100 105 110

Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu  
115 120 125

Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp  
130 135 140

Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys  
145 150 155 160

Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys  
165 170 175

Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr  
180 185 190

Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile  
195 200 205

Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu  
210 215 220

Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg  
225 230 235 240

Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu  
245 250 255

Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys  
260 265 270

Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp  
275 280 285

Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu  
290 295 300

Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala  
305 310 315 320

Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn  
325 330 335

Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu  
340 345 350

Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu  
355 360 365

Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu

370

375

380

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Lys | Pro | Phe | Gly | Asp | Phe | Met | Glu | Pro | Lys | Phe | Glu | Phe | Ala | Val |
| 385 |     |     |     | 390 |     |     |     | 395 |     |     |     |     |     |     | 400 |
| Lys | Phe | Asn | Ala | Leu | Glu | Leu | Asp | Asp | Ser | Asp | Leu | Ala | Ile | Phe | Ile |
|     |     |     |     |     |     |     |     |     | 410 |     |     |     |     |     | 415 |
| Ala | Val | Ile | Ile | Leu | Ser | Gly | Asp | Arg | Pro | Gly | Leu | Leu | Asn | Val | Lys |
|     |     |     |     |     |     |     |     | 425 |     |     |     |     |     |     | 430 |
| Pro | Ile | Glu | Asp | Ile | Gln | Asp | Asn | Leu | Leu | Gln | Ala | Leu | Glu | Leu | Gln |
|     |     |     |     |     |     |     |     | 435 |     |     |     |     |     |     | 445 |
| Leu | Lys | Leu | Asn | His | Pro | Glu | Ser | Ser | Gln | Leu | Phe | Ala | Lys | Leu | Leu |
|     |     |     |     |     |     | 450 |     |     | 455 |     |     | 460 |     |     |     |
| Gln | Lys | Met | Thr | Asp | Leu | Arg | Gln | Ile | Val | Thr | Glu | His | Val | Gln | Leu |
|     |     |     |     |     | 465 |     |     | 470 |     |     | 475 |     |     |     | 480 |
| Leu | Gln | Val | Ile | Lys | Lys | Thr | Glu | Thr | Asp | Met | Ser | Leu | His | Pro | Leu |
|     |     |     |     |     | 485 |     |     | 490 |     |     |     |     |     |     | 495 |
| Leu | Gln | Glu | Ile | Tyr | Lys | Asp | Leu | Tyr | Ala | Trp | Ala | Ile | Leu | Thr | Gly |
|     |     |     |     |     | 500 |     |     | 505 |     |     |     |     |     |     | 510 |
| Lys | Thr | Thr | Asp | Lys | Ser | Pro | Phe | Val | Ile | Tyr | Asp | Met | Asn | Ser | Leu |
|     |     |     |     |     | 515 |     |     | 520 |     |     |     |     |     |     | 525 |
| Met | Met | Gly | Glu | Asp | Lys | Ile | Lys | Phe | Lys | His | Ile | Thr | Pro | Leu | Gln |
|     |     |     |     |     | 530 |     |     | 535 |     |     | 540 |     |     |     |     |
| Glu | Gln | Ser | Lys | Glu | Val | Ala | Ile | Arg | Ile | Phe | Gln | Gly | Cys | Gln | Phe |
|     |     |     |     |     | 545 |     |     | 550 |     |     | 555 |     |     |     | 560 |
| Arg | Ser | Val | Glu | Ala | Val | Gln | Glu | Ile | Thr | Glu | Tyr | Ala | Lys | Ser | Ile |
|     |     |     |     |     | 565 |     |     | 570 |     |     |     |     |     |     | 575 |
| Pro | Gly | Phe | Val | Asn | Leu | Asp | Leu | Asn | Asp | Gln | Val | Thr | Leu | Leu | Lys |
|     |     |     |     |     | 580 |     |     | 585 |     |     |     |     |     |     | 590 |
| Tyr | Gly | Val | His | Glu | Ile | Ile | Tyr | Thr | Met | Leu | Ala | Ser | Leu | Met | Asn |
|     |     |     |     |     |     |     | 595 |     |     | 600 |     |     |     |     | 605 |
| Lys | Asp | Gly | Val | Leu | Ile | Ser | Glu | Gly | Gln | Gly | Phe | Met | Thr | Arg | Glu |
|     |     |     |     |     |     |     | 610 |     |     | 615 |     |     |     |     | 620 |
| Phe | Leu | Lys | Ser | Leu | Arg | Lys | Pro | Phe | Gly | Asp | Phe | Met | Glu | Pro | Lys |
|     |     |     |     |     | 625 |     |     | 630 |     |     | 635 |     |     |     | 640 |
| Phe | Glu | Phe | Ala | Val | Lys | Phe | Asn | Ala | Leu | Glu | Leu | Asp | Asp | Ser | Asp |
|     |     |     |     |     | 645 |     |     |     | 650 |     |     |     |     |     | 655 |

Leu Ala Ile Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly  
660 665 670

Leu Leu Asn Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln  
675 680 685

Ala Leu Glu Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu  
690 695 700

Phe Ala Lys Leu Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr  
705 710 715 720

Glu His Val Gln Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met  
725 730 735

Ser Leu His Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr  
740 745 750

<210> 4

<211> 30

<212> DNA

<213> Artificial sequence

<400> 4

GGCGATTAA ATAATGTAGT CTTATGCAAT

30

<210> 5

<211> 31

<212> DNA

<213> Artificial sequence

<400> 5

GGGGTCTAGA AGGTGCACAC CAATGTGGTG A

31